

APL-03-04PCT_Sequence_Listing
SEQUENCE LISTING

<110> Aventis Pasteur Limited
Brunham, Robert
Raudonikiene, Ausra
Galligan, Scott
Murdin, Andrew

<120> Immunization Against Chlamydia Infectio with 60K CRMP

<130> RY185

<140> US 10/580,141
<141> 2006-05-19

<150> US 60/481,676
<151> 2003-11-20

<150> PCT/CA2004/002004
<151> 2004-11-22

<160> 14

<170> PatentIn version 3.3

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<211> 1662
<212> DNA
<213> Chlamydia muridium

<220>
<221> CDS
<222> (1)..(1662)

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atc ttc gcg gtg act agt gtg gcg agt tta ttt gct agc ggg gtg tta 96
Ile Phe Ala Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu
20 25 30

gag acc tct atg gca gag tct ctc tct acc aac gtt att agc tta gct 144
Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala
35 40 45

gac acc aaa gcg aaa gag acc act tct cat caa aaa gac aga aaa gca 192
Asp Thr Lys Ala Lys Glu Thr Ser His Gln Lys Asp Arg Lys Ala
50 55 60

aga aaa aat cat caa aat agg act tcc gta gtc cgt aaa gag gtt act 240
Arg Lys Asn His Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr
65 70 75 80

gca gtt cgt gat act aaa gct gta gag cct aga cag gat tct tgc ttt 288
Ala Val Arg Asp Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe
85 90 95

ggc aaa atg tat aca gtc aaa gtt aat gat gat cgt aat gta gaa atc 336
Gly Lys Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile

APL-03-04PCT_Sequence_Listing

100	105	110	
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gag att act gct ata ggg aaa aga gac tgt gtt gat gta atc att aca Glu Ile Thr Ala Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr 130 135 140			432
cag caa tta cca tgc gaa gca gag ttt gtt agc agt gat cca gct act Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr 145 150 155 160			480
act cct act gct gat ggt aag cta gtt tgg aaa att gat cgg tta gga Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly 165 170 175			528
cag ggc gaa aag agt aaa att act gta tgg gta aaa cct ctt aaa gaa Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu 180 185 190			576
ggt tgc tgc ttt aca gct gca acg gtt tgt gct tgt cca gag atc cgt Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg 195 200 205			624
tcg gtt acg aaa tgt ggc cag cct gct atc tgt gtt aaa cag gaa ggt Ser Val Thr Lys Cys Glu Gln Pro Ala Ile Cys Val Lys Gln Glu Gly 210 215 220			672
cca gaa agc gca tgt ttg cgt tgc cca gta act tat aga att aat gta Pro Glu Ser Ala Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val 225 230 235 240			720
gtc aac caa gga aca gca aca gca cgt aat gtt gtt gtg gaa aat cct Val Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro 245 250 255			768
gtt cca gat ggc tat gct cat gca tcc gga cag cgt gta ttg aca tat Val Pro Asp Gly Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr 260 265 270			816
act ctt ggg gat atg caa cct gga gaa cag aga aca atc acc gtg gag Thr Leu Gly Asp Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu 275 280 285			864
ttt tgt ccg ctt aaa cgt ggt cga gtc aca aat att gct aca gtt tct Phe Cys Pro Leu Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser 290 295 300			912
tac tgt ggt gga cac aaa aat act gct agc gta aca aca gtg atc aat Tyr Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn 305 310 315 320			960
gag cct tgc gtg caa gtt aac atc gag gga gca gat tgg tct tat gtt Glu Pro Cys Val Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val 325 330 335			1008
tgt aag cct gta gaa tat gtt atc tct gtt tct aac cct ggt gac tta Cys Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu 340 345 350			1056
gtt tta cga gac gtt gta att gaa gat acg ctt tct cct gga ata act			1104

APL-03-04PCT_Sequence_Listing

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Val Val Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp			
370	375	380	
act ttg aag gaa ctc aat cct gga gag tct tta caa tat aag gtt cta			1200
Thr Leu Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu			
385	390	395	400
gta aga gct caa act cca ggg caa ttc aca aac aac gtt gtt gtg aaa			1248
Val Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys			
405	410	415	
agt tgc tct gat tgc ggt att tgt act tct tgc gca gaa gca aca act			1296
Ser Cys Ser Asp Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr			
420	425	430	
tac tgg aaa gga gtt gct gct act cat atg tgc gta gta gat act tgt			1344
Tyr Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys			
435	440	445	
gat cct att tgc gta gga gag aac act gtt tat cgt atc tgt gtg aca			1392
Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr			
450	455	460	
aac aga ggt tct gct gaa gat aca aat gtg tcc tta att ttg aaa ttc			1440
Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe			
465	470	475	480
tct aaa gaa tta caa cct ata tct ttc tct gga cca act aaa gga acc			1488
Ser Lys Glu Leu Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr			
485	490	495	
att aca gga aac acg gta gtg ttt gat tcg tta cct aga tta ggt tct			1536
Ile Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser			
500	505	510	
aaa gaa act gta gag ttt tct gta acg ttg aaa gca gta tcc gct gga			1584
Lys Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly			
515	520	525	
gat gct cgt ggg gaa gct att ctt tct tcc gat aca ttg aca gtt cct			1632
Asp Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro			
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545	550		

<210> 2
<211> 554
<212> PRT
<213> Chlamydia muridium

<400> 2

Met Arg Ile Gly Asp Pro Met Asn Lys Leu Ile Arg Arg Ala Val Thr
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APL-03-04PCT_Sequence_Listing

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20 25 30

Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala
35 40 45

Asp Thr Lys Ala Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala
50 55 60

Arg Lys Asn His Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr
65 70 75 80

Ala Val Arg Asp Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe
85 90 95

Gly Lys Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile
100 105 110

Val Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile
115 120 125

Glu Ile Thr Ala Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr
130 135 140

Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr
145 150 155 160

Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly
165 170 175

Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu
180 185 190

Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg
195 200 205

Ser Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly
210 215 220

Pro Glu Ser Ala Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val
225 230 235 240

Val Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro
245 250 255

Val Pro Asp Gly Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr
260 265 270

APL-03-04PCT_Sequence_Listing

Thr Leu Gly Asp Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu
275 280 285

Phe Cys Pro Leu Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser
290 295 300

Tyr Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn
305 310 315 320

Glu Pro Cys Val Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val
325 330 335

Cys Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu
340 345 350

Val Leu Arg Asp Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr
355 360 365

Val Val Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp
370 375 380

Thr Leu Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu
385 390 395 400

Val Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Lys
405 410 415

Ser Cys Ser Asp Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr
420 425 430

Tyr Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys
435 440 445

Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr
450 455 460

Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe
465 470 475 480

Ser Lys Glu Leu Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr
485 490 495

Ile Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser
500 505 510

Lys Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly
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APL-03-04PCT_Sequence_Listing

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Val Ser Asp Thr Glu Asn Thr His Ile Tyr
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gag acc tct atg gca gag tct ctc tct aca aac gtt att agc tta gct 144
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 35 40 45

gac acc aaa gcg aaa gac aac act tct cat aaa agc aaa aaa gca aga 192
 Asp Thr Lys Ala Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg
 50 55 60

aaa aac cac agc aaa gag act ccc gta gac cgt aaa gag gtt gct ccg 240
Lys Asn His Ser Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro
65 70 75 80

gtt cat gag tct aaa gct aca gga cct aaa cag gat tct tgc ttt ggc 288
 Val His Glu Ser Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly
 85 90 95

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aga atg tat aca gtc aaa gtt aat gat gat cgc aat gtt gaa atc aca      336
Arg Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr
          100          105          110

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caa gct gtt cct gaa tat gct acg gta gga tct ccc tat cct att gaa 384
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 115 120 125

att act gct aca ggt aaa agg gat tgt gtt gat gtt atc att act cag
Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln
130 135 140

caa tta cca tgt gaa gca gag ttc gta cgc agt gat cca gcg aca act
 Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr
 145 150 155 160

cct act gct gat ggt aag cta gtt tgg aaa att gac cgc tta gga caa
 Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln 528

APL-03-04PCT_Sequence_Listing

165

170

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tgc tgc ttt aca gct gca aca gta tgc gct tgt cca gag atc cgt tcg Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser 195 200 205	624
gtt aca aaa tgt gga caa cct gct atc tgt gtt aaa caa gaa ggc cca Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro 210 215 220	672
gag aat gct tgt ttg cgt tgc cca gta gtt tac aaa att aat ata gtg Glu Asn Ala Cys Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val 225 230 235 240	720
aac caa gga aca gca aca gct cgt aac gtt gtt gaa aat cct gtt Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val 245 250 255	768
cca gat ggt tac gct cat tct tct gga cag cgt gta ctg acg ttt act Pro Asp Gly Tyr Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr 260 265 270	816
ctt gga gat atg caa cct gga gag cac aga aca att act gta gag ttt Leu Gly Asp Met Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe 275 280 285	864
tgt ccg ctt aaa cgt ggt cgt gct acc aat ata gca acg gtt tct tac Cys Pro Leu Lys Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr 290 295 300	912
tgt gga gga cat aaa aat aca gca agc gta aca act gtg atc aac gag Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu 305 310 315 320	960
cct tgc gta caa gta agt att gca gga gca gat tgg tct tat gtt tgt Pro Cys Val Gln Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys 325 330 335	1008
aag cct gta gaa tat gtg atc tcc gtt tcc aat cct gga gat ctt gtg Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val 340 345 350	1056
ttg cga gat gtc gtc gtt gaa gac act ctt tct ccc gga gtc aca gtt Leu Arg Asp Val Val Val Glu Asp Thr Leu Ser Pro Gly Val Thr Val 355 360 365	1104
ctt gaa gct gca gga gct caa att tct tgt aat aaa gta gtt tgg act Leu Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Val Val Trp Thr 370 375 380	1152
gtg aaa gaa ctg aat cct gga gag tct cta cag tat aaa gtt cta gta Val Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val 385 390 395 400	1200
aga gca caa act cct gga caa ttc aca aat aat gtt gtt gtg aag agc Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser 405 410 415	1248
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APL-03-04PCT_Sequence_Listing

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Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp			
435	440	445	
cct gtt tgt gta gga gaa aat act gtt tac cgt att tgt gtc acc aac			1392
Pro Val Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn			
450	455	460	
aga ggt tct gca gaa gat aca aat gtt tct tta atg ctt aaa ttc tct			1440
Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser			
465	470	475	480
aaa gaa ctg caa cct gta tcc ttc tct gga cca act aaa gga acg att			1488
Lys Glu Leu Gln Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile			
485	490	495	
aca ggc aat aca gta gta ttc gat tcg tta cct aga tta ggt tct aaa			1536
Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys			
500	505	510	
gaa act gta gag ttt tct gta aca ttg aaa gca gta tca gct gga gat			1584
Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp			
515	520	525	
gct cgt ggg gaa gcg att ctt tct tcc gat aca ttg act gtt cca gtt			1632
Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val			
530	535	540	
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Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala			
35	40	45	
Asp Thr Lys Ala Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg			
50	55	60	
Lys Asn His Ser Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro			
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APL-03-04PCT_Sequence_Listing

Val His Glu Ser Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly
 85 90 95

Arg Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr
 100 105 110

Gln Ala Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu
 115 120 125

Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln
 130 135 140

Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr
 145 150 155 160

Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln
 165 170 175

Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
 180 185 190

Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser
 195 200 205

Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro
 210 215 220

Glu Asn Ala Cys Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val
 225 230 235 240

Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val
 245 250 255

Pro Asp Gly Tyr Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr
 260 265 270

Leu Gly Asp Met Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe
 275 280 285

Cys Pro Leu Lys Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr
 290 295 300

Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu
 305 310 315 320

Pro Cys Val Gln Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys
 325 330 335

APL-03-04PCT_Sequence_Listing

Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val
340 345 350

Leu Arg Asp Val Val Val Glu Asp Thr Leu Ser Pro Gly Val Thr Val
355 360 365

Leu Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Val Val Trp Thr
370 375 380

Val Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val
385 390 395 400

Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser
405 410 415

Cys Ser Asp Cys Gly Thr Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr
420 425 430

Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp
435 440 445

Pro Val Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn
450 455 460

Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser
465 470 475 480

Lys Glu Leu Gln Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile
485 490 495

Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys
500 505 510

Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp
515 520 525

Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val
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Ser Asp Thr Glu Asn Thr His Ile Tyr
545 550

<210> 5
<211> 1554

<212> DNA

<213> Chlamydia muridium

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aaa gag acc act tct cat caa aaa gac aga aaa gca aga aaa aat cat		96
Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala Arg Lys Asn His		
20 25 30		
caa aat agg act tcc gta gtc cgt aaa gag gtt act gca gtt cgt gat		144
Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr Ala Val Arg Asp		
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Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe Gly Lys Met Tyr		
50 55 60		
aca gtc aaa gtt aat gat gat cgt aat gta gaa atc gtg cag tcc gtt		240
Thr Val Lys Val Asn Asp Arg Asn Val Glu Ile Val Gln Ser Val		
65 70 75 80		
cct gaa tat gct acg gta gga tct cca tat cct att gag att act gct		288
Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala		
85 90 95		
ata ggg aaa aga gac tgt gtt gat gta atc att aca cag caa tta cca		336
Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro		
100 105 110		
tgc gaa gca gag ttt gtt agc agt gat cca gct act act cct act gct		384
Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr Thr Pro Thr Ala		
115 120 125		
gat ggt aag cta gtt tgg aaa att gat cggtt gga cag ggc gaa aag		432
Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys		
130 135 140		
agt aaa att act gta tgg gta aaa cct ctt aaa gaa ggt tgc tgc ttt		480
Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe		
145 150 155 160		
aca gct gca acg gtt tgt gct tgt cca gag atc cgt tcg gtt acg aaa		528
Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser Val Thr Lys		
165 170 175		
tgt ggc cag cct gct atc tgt gtt aaa cag gaa ggt cca gaa agc gca		576
Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro Glu Ser Ala		
180 185 190		
tgt ttg cgt tgc cca gta act tat aga att aat gta gtc aac caa gga		624
Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val Val Asn Gln Gly		
195 200 205		
aca gca aca gca cgt aat gtt gtt gtg gaa aat cct gtt cca gat ggc		672
Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly		
210 215 220		
tat gct cat gca tcc gga cag cgt gta ttg aca tat act ctt ggg gat		720
Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr Thr Leu Gly Asp		

APL-03-04PCT_Sequence_Listing

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aaa cgt ggt cga gtc aca aat att gct aca gtt tct tac tgt ggt gga Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser Tyr Cys Gly Gly	260	265	270	816
cac aaa aat act gct agc gta aca aca gtg atc aat gag cct tgc gtg His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu Pro Cys Val	275	280	285	864
caa gtt aac atc gag gga gca gat tgg tct tat gtt tgt aag cct gta Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val	290	295	300	912
gaa tat gtt atc tct gtt tct aac cct ggt gac tta gtt tta cga gac Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val Leu Arg Asp	305	310	315	960
gtt gta att gaa gat acg ctt tct cct gga ata act gtt gtt gaa gca Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr Val Val Glu Ala	325	330	335	1008
gct gga gct cag att tct tgt aat aaa ttg gtt tgg act ttg aag gaa Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp Thr Leu Lys Glu	340	345	350	1056
ctc aat cct gga gag tct tta caa tat aag gtt cta gta aga gct caa Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln	355	360	365	1104
act cca ggg caa ttc aca aac aac gtt gtt gtg aaa agt tgc tct gat Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp	370	375	380	1152
tgc ggt att tgt act tct tgc gca gaa gca aca act tac tgg aaa gga Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly	385	390	395	400
gtt gct gct act cat atg tgc gta gta gat act tgt gat cct att tgc Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Ile Cys	405	410	415	1248
gta gga gag aac act gtt tat cgt atc tgt gtg aca aac aga ggt tct Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser	420	425	430	1296
gct gaa gat aca aat gtg tcc tta att ttg aaa ttc tct aaa gaa tta Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe Ser Lys Glu Leu	435	440	445	1344
caa cct ata tct ttc tct gga cca act aaa gga acc att aca gga aac Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn	450	455	460	1392
acg gta gtg ttt gat tcg tta cct aga tta ggt tct aaa gaa act gta Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val	465	470	475	1440
gag ttt tct gta acg ttg aaa gca gta tcc gct gga gat gct cgt ggg				1488

APL-03-04PCT_Sequence_Listing

Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly
485 490 495

gaa gct att ctt tct tcc gat aca ttg aca gtt cct gta tct gat acg 1536
Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr
500 505 510

gag aat aca cat atc tat 1554
Glu Asn Thr His Ile Tyr
515

<210> 6
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<212> PRT
<213> Chlamydia muridium

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Met Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala Asp Thr Lys Ala
1 5 10 15

Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala Arg Lys Asn His
20 25 30

Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr Ala Val Arg Asp
35 40 45

Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe Gly Lys Met Tyr
50 55 60

Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Val Gln Ser Val
65 70 75 80

Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala
85 90 95

Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro
100 105 110

Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr Thr Pro Thr Ala
115 120 125

Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys
130 135 140

Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe
145 150 155 160

Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser Val Thr Lys
165 170 175

APL-03-04PCT_Sequence_Listing

Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro Glu Ser Ala
180 185 190

Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val Val Asn Gln Gly
195 200 205

Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly
210 215 220

Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr Thr Leu Gly Asp
225 230 235 240

Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu Phe Cys Pro Leu
245 250 255

Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser Tyr Cys Gly Gly
260 265 270

His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu Pro Cys Val
275 280 285

Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val
290 295 300

Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val Leu Arg Asp
305 310 315 320

Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr Val Val Glu Ala
325 330 335

Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp Thr Leu Lys Glu
340 345 350

Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln
355 360 365

Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp
370 375 380

Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly
385 390 395 400

Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Ile Cys
405 410 415

Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser
420 425 430

APL-03-04PCT_Sequence_Listing

Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe Ser Lys Glu Leu
 435 440 445

Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn
 450 455 460

Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val
 465 470 475 480

Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly
 485 490 495

Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr
 500 505 510

Glu Asn Thr His Ile Tyr
 515

<210> 7
 <211> 1551
 <212> DNA
 <213> Chlamydia trachomatis

<220>
 <221> CDS
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<400> 7		
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1 5 10 15		
aaa gac aac act tct cat aaa agc aaa aaa gca aga aaa aac cac agc		96
Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg Lys Asn His Ser		
20 25 30		
aaa gag act ccc gta gac cgt aaa gag gtt gct ccg gtt cat gag tct		144
Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro Val His Glu Ser		
35 40 45		
aaa gct aca gga cct aaa cag gat tct tgc ttt ggc aga atg tat aca		192
Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly Arg Met Tyr Thr		
50 55 60		
gtc aaa gtt aat gat gat cgc aat gtt gaa atc aca caa gct gtt cct		240
Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr Gln Ala Val Pro		
65 70 75 80		
gaa tat gct acg gta gga tct ccc tat cct att gaa att act gct aca		288
Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala Thr		
85 90 95		
ggt aaa agg gat tgt gtt gat gtt atc att act cag caa tta cca tgt		336
Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro Cys		
100 105 110		

APL-03-04PCT_Sequence_Listing

gaa gca gag ttc gta cgc agt gat cca gcg aca act cct act gct gat Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala Asp 115 120 125	384
ggt aag cta gtt tgg aaa att gac cgc tta gga caa ggc gaa aag agt Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys Ser 130 135 140	432
aaa att act gta tgg gta aaa cct ctt aaa gaa ggt tgc tgc ttt aca Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe Thr 145 150 155 160	480
gct gca aca gta tgc gct tgt cca gag atc cgt tcg gtt aca aaa tgt Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser Val Thr Lys Cys 165 170 175	528
gga caa cct gct atc tgt gtt aaa caa gaa ggc cca gag aat gct tgt Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro Glu Asn Ala Cys 180 185 190	576
ttg cgt tgc cca gta gtt tac aaa att aat ata gtg aac caa gga aca Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val Asn Gln Gly Thr 195 200 205	624
gca aca gct cgt aac gtt gtt gtt gaa aat cct gtt cca gat ggt tac Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly Tyr 210 215 220	672
gct cat tct tct gga cag cgt gta ctg acg ttt act ctt gga gat atg Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr Leu Gly Asp Met 225 230 235 240	720
caa cct gga gag cac aga aca att act gta gag ttt tgt ccg ctt aaa Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe Cys Pro Leu Lys 245 250 255	768
cgt ggt cgt gct acc aat ata gca acg gtt tct tac tgt gga gga cat Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr Cys Gly Gly His 260 265 270	816
aaa aat aca gca agc gta aca act gtg atc aac gag cct tgc gta caa Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu Pro Cys Val Gln 275 280 285	864
gta agt att gca gga gca gat tgg tct tat gtt tgt aag cct gta gaa Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val Glu 290 295 300	912
tat gtg atc tcc gtt tcc aat cct gga gat ctt gtg ttg cga gat gtc Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val Leu Arg Asp Val 305 310 315 320	960
gtc gtt gaa gac act ctt tct ccc gga gtc aca gtt ctt gaa gct gca Val Val Glu Asp Thr Leu Ser Pro Gly Val Thr Val Leu Glu Ala Ala 325 330 335	1008
gga gct caa att tct tgt aat aaa gta gtt tgg act gtg aaa gaa ctg Gly Ala Gln Ile Ser Cys Asn Lys Val Val Trp Thr Val Lys Glu Leu 340 345 350	1056
aat cct gga gag tct cta cag tat aaa gtt cta gta aga gca caa act Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln Thr	1104

APL-03-04PCT_Sequence_Listing
 355 360 365

cct gga caa ttc aca aat aat gtt gtt gtg aag aac tgc tct gac tgt Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp Cys 370 375 380	1152
ggt act tgt act tct tgc gca gaa gcg aca act tac tgg aaa gga gtt Gly Thr Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly Val 385 390 395 400	1200
gct gct act cat atg tgc gta gta gat act tgt gac cct gtt tgt gta Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Val Cys Val 405 410 415	1248
gga gaa aat act gtt tac cgt att tgt gtc acc aac aga ggt tct gca Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser Ala 420 425 430	1296
gaa gat aca aat gtt tct tta atg ctt aaa ttc tct aaa gaa ctg caa Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser Lys Glu Leu Gln 435 440 445	1344
cct gta tcc ttc tct gga cca act aaa gga acg att aca ggc aat aca Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn Thr 450 455 460	1392
gta gta ttc gat tcg tta cct aga tta ggt tct aaa gaa act gta gag Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val Glu 465 470 475 480	1440
ttt tct gta aca ttg aaa gca gta tca gct gga gat gct cgt ggg gaa Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly Glu 485 490 495	1488
gcg att ctt tct tcc gat aca ttg act gtt cca gtt tct gat aca gag Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr Glu 500 505 510	1536
aat aca cac atc tat Asn Thr His Ile Tyr 515	1551

<210> 8
 <211> 517
 <212> PRT
 <213> Chlamydia trachomatis

<400> 8

Met Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala Asp Thr Lys Ala
 1 5 10 15

Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg Lys Asn His Ser
 20 25 30

Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro Val His Glu Ser
 35 40 45

Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly Arg Met Tyr Thr
 Page 17

APL-03-04PCT_Sequence_Listing

50

55

60

Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr Gln Ala Val Pro
65 70 75 80

Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala Thr
85 90 95

Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro Cys
100 105 110

Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala Asp
115 120 125

Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys Ser
130 135 140

Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe Thr
145 150 155 160

Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser Val Thr Lys Cys
165 170 175

Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro Glu Asn Ala Cys
180 185 190

Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val Asn Gln Gly Thr
195 200 205

Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly Tyr
210 215 220

Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr Leu Gly Asp Met
225 230 235 240

Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe Cys Pro Leu Lys
245 250 255

Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr Cys Gly Gly His
260 265 270

Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu Pro Cys Val Gln
275 280 285

Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val Glu
290 295 300

APL-03-04PCT_Sequence_Listing

Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val Leu Arg Asp Val
305 310 315 320

Val Val Glu Asp Thr Leu Ser Pro Gly Val Thr Val Leu Glu Ala Ala
325 330 335

Gly Ala Gln Ile Ser Cys Asn Lys Val Val Trp Thr Val Lys Glu Leu
340 345 350

Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln Thr
355 360 365

Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp Cys
370 375 380

Gly Thr Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly Val
385 390 395 400

Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Val Cys Val
405 410 415

Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser Ala
420 425 430

Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser Lys Glu Leu Gln
435 440 445

Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn Thr
450 455 460

Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val Glu
465 470 475 480

Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly Glu
485 490 495

Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr Glu
500 505 510

Asn Thr His Ile Tyr
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<213> Chlamydia muridium

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APL-03-04PCT_Sequence_Listing

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<210> 13
<211> 31
<212> DNA
<213> Chlamydia muridium

<400> 13 gaattcggat ccgatgaaca aactcatcag a 31

<210> 14
<211> 36
<212> DNA
<213> Chlamydia muridium

<400> 14 attaagaatg cggccgcttc attaatagat atgtgt 36